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Brain abscess, epidemiology, clinical manifestations and management

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Background: Infection involving the cerebrum is a true neurosurgical emergency that requires rapid diagnosis and appropriate surgical and medical intervention to achieve good clinical outcome.

Methods: In this study we evaluated 41 pateints with brain abscess in our hospital in during 2005-2010. Demographic information, predisposing factors, clinical manifestations, lab. data and managements were evaluated.

Results: In this study %53.6 of patients were 15-29 years old, %26 were 30-49 and %17 were 50-70 years old. Clinical manifestation was as follow in our study:

Headache %92.6, nausea and vomiting %73.1, meningeal signs %17, drowsiness %12, decreased level of consciousness %9.7, fever %9.7, uninary and fecal incontinency % 7.3, visual disturbance % 7.3, chills %4.8. Predisposing condition leading to brain abscess in our study were sinusitis in %9.17, otitis in % 12, CSF rhinorrhea in % 2.4, mastoiditis in % 7.2, neurosurgery in % 17 and endocaiditis in %2.4. %20 of our patients had no risk factor. Antibiotics used in our study were ceftriaxne, metronidazole and vancomycin. Mortality rate was %12 in this study. % 9.7 of our patient that were admitted with diagnosis of brain abscess finally diagnosed as they had acute demyelinating encephalomyelitis (ADEM).

Conclusion: With promp diagnosis and treatment most cases of brain abscess survived. Few cases initially diagnosed as brain abscess may have other diagnosis like acute demyelinating encephalomyelitis (ADEM).

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A long–term antimicrobial prophylaxis and/or immunotherapy in female patients with recurrent urinary tract infections

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Background: It is accepted that long-term low-dose antimicrobial prophylaxis decreases recurrence of urinary tract infections (UTI). In recent years, the oral administration of immunotherapy has been used as an alternative to long–term preventive effect of chemoprophylaxis with low-dose fluoroquinolones and/or immunotherapy in women with recurrent UTI. Both Uro–Vaxom (OM – 89) and Luivac are extracts of bacterial components with complex immunostimulating activity.

Methods: Adult female patients with at least 3 documented episodes of UTI in previous year were enrolled in this 12-months, multicenter study. Patients received continuous chemoprophylaxis with low–dose ciprofloxacin and/or immunotherapy with either Uro-Vaxom or Luivac. Primary efficacy criteria were UTI episodes over the 12 months treatment period.

Results: A total of 178 patients were treated, 89 in the Uro–Vaxom and 89 in the Luivac group, respectively. Mean rate of post baseline UTIs decreased significantly in both treatment groups: in Uro–Vaxom group from 3.54 to 0.48 episode/patient/year and in Luivac group from 3.63 to 0.41 episode/patient/year, $p < 0.001$. There were 67.1% patients treated with combination of immunotherapy and quinolone prophylaxis vs. 52.7% patients treated with immunotherapy only, who were UTI–free in 12–months study period ($p = 0.04$). In the subgroup receiving continuous antimicrobial prophylaxis with ciprofloxacin (125 mg orally every other day), selection of quinolone-resistant strains was observed in 9 patients (ESBL–producing strains of *E. coli* and *Klebsiella pneumoniae*).

Conclusion: These results confirm that immunotherapy is more safe and almost as effective as low-dose quinolone prophylaxis in prevention of recurrent UTI. Selection of quinolone–resistant strains is a potential threat for patients on long-term treatment with fluoroquinolones.

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Multilocus sequencing analysis of viridans group streptococci isolated from patients with infective endocarditis

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Background: Infective endocarditis (IE) is a serious infection associated with considerable morbidity and mortality. About 44% of the IE cases are commonly due to a heterogeneous group of organisms, which are the part of commensal flora of the upper respiratory tract in humans called viridans group streptococci (VGS). Each species of VGS possesses variable pathogenicity and virulence potential, hence, accurate identification of VGS to the species level is important. The taxonomy of these organisms has been always perplexing, and accurate identification of VGS remains a challenge due to the high degree of similarity between members of the groups. Very closely related species of VGS can be identified from other species using the concatenated sequences of multiple core (house-keeping) genes known as Multilocus Sequencing Analysis (MLSA). More recently, a MLSA technique has been developed for identification of VGS based on the nucleotide sequence analysis of seven house-keeping genes. Hence, this study was aimed to assess the reliability and discriminate efficiency of MLSA for the identification of VGS.

Methods: MLSA was done for 48 strains of VGS isolated from blood cultures of patients with IE by using concatenated sequences of the seven house-keeping genes map, pfl, pyk, ppaC, rpoB, soda, and tuf (http://www.eMLSA.net),. Nucleotide alignments and phylogenetic trees were constructed with the neighbour-joining method using single house-keeping genes and concatenated sequences of seven house-keeping genes in MEGA version 5.0.

Results: Analysis of 36 strains out of 48 VGS was done, since six *Streptococcus oralis* did not reach the required sequence length for the *sodA* gene when analysed by the MLSA software, and one *Streptococcus mutans* and five *Streptococcus sanguinis* did not amplify *map* gene by PCR. All the sequence clusters could be equated with recognized species and based on MLSA, twenty one were identified as *Streptococcus oralis*, six as *Streptococcus gordonii*, five as *Streptococcus sanguinis*, three as *Streptococcus parasanguinis*, and one as *Streptococcus anginosus*.

Conclusion: Results of MLSA revealed that the closely related species of VGS fall into well-resolved clusters when compared to single gene-based identification.

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Genetic diversity of Malaysian methicillin resistant *Staphylococcus aureus* strains based on virulotypes, pulsed-field gel electrophoresis and PCR-RFLP of coa gene

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Background: *Staphylococcus aureus* is a persistent human pathogen responsible for a variety of infections ranging from soft-tissue infections to bacteremia. The objective of this study was to determine the prevalence of a repertoire of toxin genes among Malaysian MRSA strains isolated over a four years period and the genetic relatedness of MRSA strains.

Methods: One hundred eighty-eight strains (2003, 2004, 2007 and 2008) of methicillin-resistant *S. aureus* (MRSA) isolated from a tertiary hospital were screened for 20 genes encoding for extracellular virulence determinant (*sea, seb, sec, sed, see, seg, seh, sei, sej, tst, eta, etb,etd*) and adhesins (*cna, etb, fnbA, fnbB, hlg, ica, sdrE*) via PCR. The genetic relatedness of these strains was determined by PFGE, PCR-RFLP of *coa* gene and *agr* grouping.

Results: Majority of the strains were tested positive for *efb* and *fnbA* (96% each), *ica* (78%) and *hlg* (59%) genes. A total of 101 strains were positive for at least one type of staphylococcal enterotoxin genes with *sea* being the predominant. Genes for *seb, sed, see, seh, sej, eta* and *etb* were not detected in any of the MRSA strains. The prevalence of *sea*, *sec* and *ica* among strains isolated in 2008 was increased significantly ($p < 0.05$) compared to 2003. Most of the strains were of *agr* type I (97.5%) followed by *agr* type II (1.2%) and *agr* type III (0.6%). Subtyping by PFGE and PCR-RFLP of coa gene produce 88 different pulsed-field profiles (F = 0.51-1.0) and 47 different patterns (F = 0.24-1.0), respectively.

Conclusion: No direct correlation between virulotypes, PFGE and PCR-RFLP profiles was observed. Strains with identical PFGE and PCR-RFLP profiles frequently belonged to different virulence patterns. Increase of MRSA strains with virulence factors over the years signal the potential loss of the usage of antimicrobial agents in treating MRSA infections as MRSA strains with virulence factors are normally resistant to host immune systems and other antimicrobial agents. The MRSA clinical strains from this tertiary hospital were genetically related, suggesting that few predominant clones of the species are involved in infections.

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Aetiological agents of meningitis in Zambia: Is there a need for a pneumococcal vaccine?

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Background: Meningitis continues to be a major cause of morbidity and mortality in Zambia. This is a problem more especially in HIV/AIDS patients and the paediatric age group. Because of the higher risk of mortality in the under five age group, the Zambian government with the aid of the World Health Organisation has an on-going surveillance of Paediatric Bacterial Meningitis (PBM) to determine the causative agents. The data is for patient management as well as policy decisions such as introduction of vaccines for immunisation against pneumonia and meningitis. The country is in the process of introducing a pneumococcal vaccine and therefore requires information on serotypes to decide on whether to introduce 7, 10, 13 or 23 valent pneumococcal vaccines.

The University Teaching Hospital Microbiology (UTH) laboratory, Lusaka, receives over two thousand Cerebral Spinal Fluid specimens for the diagnosis of meningitis. The microbiological procedures include microscopy examination (cell count, India ink and Gram staining). Samples are also cultured for bacterial and fungal pathogens and antimicrobial susceptibility testing by the Buaer-Kirby and MIC methods.

Methods: The UTH laboratory data for the year 2011 was reviewed to determine the main causative agents of meningitis, and the antimicrobial susceptibility. Some strains (17) of Streptococcus pneumoniawere serotyped at the National Institute of Infectious Diseases (NICD), South Africa.

Results: About 90% of all specimens suggest aseptic meningitis. The positive cultures included the fungal agentCryptococcus neoformans (42%)and bacterial pathogens wereStreptococcus pneumonia (37%), Neisseria meningitides (5%),Salmonella Typhi (2%)and other organisms. The pneumococcal serotypes identified included 1, 4, 6A, 6B, 7F, 10F, 15C, 19A, and 23F. More than 23% of Streptococcuspneumoniaewas isolated from the paediatric age group though all age groups were affected. The antibiotic resistance of 17strains ofS.pneumoniaetoChloramphenicol (Buaer-Kirby), Penicillin (MIC 0.12-1.00 μg/ml), and Cefotaxime (MIC≤0.5 μg/ml) were 41%, 23%, and 0% respectively.

Conclusion: Despite the introduction of Antiretroviral drugs (HAART), Cryptococcus continues to be a common opportunistic infection in HIV/AIDs patients in Zambia. S. pneumoniaeis the major